

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

Listing of The Claims:

What is claimed is:

1. (original) A method of diagnosing or prognosing a disease in an individual, comprising the steps of:

a) determining the level of expression of a gene in a blood sample of an individual, and

b) detecting a difference of said level of expression of said gene in said blood sample according to step a) relative to the level of expression of the same gene of a control, wherein a difference in expression levels is indicative or predictive of said disease.

2. (original) A method of diagnosing or prognosing a disease in an individual, comprising the steps of:

a) determining the level of expression of a gene in a blood sample of an individual; and

b) detecting the same level of expression of said gene in said blood sample according to step a) relative to the level of expression of the same gene of a control, wherein the same level of expression is indicative or predictive of said disease.

3. (original) The method of claim 1, wherein said control is a non-disease control.

4. (original) The method of claim 2, wherein said control is a disease control.

5. (original) The method of claims 1 or 2, wherein said control is from a blood sample of one or more individuals.

6. (original) The method of claims 1 or 2, wherein said control is from a blood sample of one or more individuals undergoing treatment for a disease.

7. (currently amended) A method of identifying a disease marker useful for diagnosing a disease, comprising the steps of:

a) detecting the presence of RNA encoded by a gene expressed in blood and in a non-blood tissue of a subject not having said disease, in an unfractionated sample of whole blood from each of one or more subjects having said disease, and quantifying a level of said RNA in said sample~~determining the level of expression of a gene in a blood sample of an individual having a disease, wherein said gene is a candidate disease marker~~; and

b) determining a difference between said level and a quantified level of control RNA from an unfractionated sample of whole blood from each of one or more first control subjects, said control RNA being encoded by said gene and being detectable in said sample from said control subjects, said~~comparing said level of said step a) with the level of expression of said gene in an individual not having said disease, wherein a difference~~ identifying ~~in said levels~~ identifies said ~~candidate~~ gene as a marker of said disease.

8. (currently amended) A method of identifying a disease marker useful for diagnosing a disease, comprising the steps of:

a) producing an amplification product from RNA extracted from an unfractionated sample of whole blood from each of one or more subjects~~determining the level of expression of a gene in a blood sample of an individual having a said disease, said amplification product being encoded by~~ wherein said gene is a candidate disease marker and said gene corresponds to a gene expressed in blood and in a non-blood tissue of a subject not having said disease, and quantifying said amplification product; and

b) determining a difference between said quantity of said amplification product and a quantity of an amplification product from control RNA, said control RNA being extracted from an unfractionated sample of whole blood from each of one or more control subjects, said amplification product from said control RNA being encoded by said gene, and expression of said gene being detectable in said sample from said each of one or more control subjects, comparing~~said level of said step a) with the level of expression of said gene in an individual not having said~~

disease, wherein a said difference in said levels identifies said candidate gene as a marker of said disease.

9. (currently amended) A The method of claim 7 or claim 8, wherein said subjects having said disease are asymptomatic with respect to said disease of identifying a gene as marker for disease progression, comprising the steps of:

a) ~~determining the level of expression of a gene in a blood sample of an individual having a symptom of a disease, wherein said gene is a candidate for determining disease progression;~~
and

b) ~~comparing said level of said step a) with the level of expression of a corresponding gene of an individual not having said symptom or having a different symptom, wherein a difference in said levels identifies said candidate gene as a marker of disease progression.~~

10. (currently amended) A The method of claim 7 or claim 8, wherein said of identifying a gene is as a marker for disease progression, comprising the steps of:

a) ~~determining the level of expression of a gene in a blood sample of an individual having a symptom of a disease, wherein said gene is a candidate for determining disease progression and said gene corresponds to a gene expressed in non blood tissue; and~~

b) ~~comparing said level of said step a) with the level of expression of a corresponding gene of an individual not having said disease, wherein a difference in said levels identifies said candidate gene as a marker of disease progression.~~

11. (canceled)

12. (canceled)

13. (currently amended) The method of claim 7 or 8, claims 1, 2, 7, 8, 9, 10 or 11, wherein said disease is selected from the group consisting of diabetes and heart failure~~coronary artery disease.~~

14. (canceled)

15. (canceled)

16. (currently amended) The method of claim 7 or 8, ~~claims 1, 2, 7, 8, 9, 10-11 or 12,~~ wherein said blood sample from each of said one or more subjects having said disease is a drop of blood.

17. (currently amended) The method of claim 7, ~~claims 1, 2, 7, 8, 9, 10-11 or 12,~~ ~~wherein in said step a)~~ said level of expression is determined for two or more genes further comprising:

(c) in said sample of step (a): detecting an RNA encoded by a second gene, said second gene being distinct from said gene in step (a) and being expressed in blood and in a non-blood tissue of said subject not having said disease; and quantifying a level of said RNA encoded by said second gene; and

(d) determining, in an unfractionated sample of whole blood from each of one or more second control subjects, a difference between: said level of said RNA encoded by said second gene, and a quantified level of a control RNA being encoded by said second gene, and being detectable in said sample from said second control subjects, wherein said difference between: said level of said RNA encoded by said second gene; and said quantified level of said control RNA being encoded by said second gene identifies said second gene as a further marker of said disease.

18. (canceled)

19. (New) The method of claim 8, further comprising:

(c) producing from said RNA of step (a) an amplification product encoded by a second gene, said second gene being distinct from said gene of step (a) and being expressed in blood and in non-blood tissue of said subject not having said disease; and quantifying a level of said amplification product encoded by said second gene; and

(d) determining a difference between a quantity of said amplification product of step (c) and a quantity of an amplification product from reference RNA, said reference RNA being extracted from an unfractionated sample of whole blood from each of one or more reference subjects, said amplification product from reference RNA being encoded by said second gene, and expression of said second gene being detectable in said sample from said each of one or more reference subjects, wherein said difference of step (d) identifies said second gene as a further marker of said disease.

20. (New) The method of claim 7, wherein said detecting of said RNA of step (a) is effected by detecting cDNA and/or EST derived from said RNA of step (a).

21. (New) The method of claim 8, wherein said producing of said amplification product of said RNA of step (a) is effected by producing an amplification product of cDNA and/or EST derived from said RNA of step (a).

22. (New) The method of claim 8, wherein said producing of said amplification product of step (a) is effected by producing an amplification product of cDNA and/or EST derived from said RNA of step (a) using primers specific for said gene.

23. (New) The method of claim 7, further comprising:

- (c) quantifying a level of said control RNA in said sample of step (b) to thereby determine said quantified level of said control RNA.

24. (New) The method of claim 8, further comprising:

- (c) quantifying a level of said amplification product from said control RNA in said sample of step (b) to thereby determine said quantity of said amplification product from said control RNA.

25. (New) The method of claim 7, further comprising:

- (c) isolating and quantifying said control RNA to thereby determine said quantified level of said control RNA.

26. (New) The method of claim 8, further comprising:

- (c) isolating and quantifying said amplification product from said control RNA to thereby determine said quantity of said amplification product from said control RNA.

27. (New) The method of claim 7, wherein the method further comprises isolating said RNA of step (a) prior to said detecting of said RNA of step (a).

28. (New) The method of claim 7, wherein said quantifying of said level of said RNA of step (a) is effected by determining a quantity of said RNA of step (a) relative to a quantity of a housekeeping gene.

29. (New) The method of claim 7, wherein said quantifying of said level of said control RNA is effected by determining a quantity of said control RNA relative to a quantity of a housekeeping gene.

30. (New) The method of claim 8, wherein said quantifying of said amplification product from said RNA of step (a) is effected by determining a quantity of said amplification product from said RNA of step (a) relative to a quantity of a housekeeping gene.

31. (New) The method of claim 8, wherein said quantifying of said amplification product from said control RNA is effected by determining a quantity of said amplification product from said control RNA relative to a quantity of a housekeeping gene.

32. (New) The method of claim 7 or 8, wherein said each of said one or more subjects having said disease, said subject not having said disease and/or each of said one or more control subjects is a human.

33. (New) The method of claim 17, wherein said each of said one or more subjects having said disease, said subject not having said disease, said each of said one or more first control subjects and/or said each of said one or more second control subjects is a human.

34. (New) The method of claim 7 or 8, wherein none of said one or more control subjects have said disease.

35. (New) The method of claim 17, wherein none of said one or more first control subjects and/or none of said one or more second control subjects have said disease.

36. (New) The method of claim 7 or 8, wherein said sample from each of said one or more control subjects is a drop of blood.

37. (New) The method of claim 17, wherein said sample from each of said one or more first control subjects and/or said sample from each of said one or more second control subjects is a drop of blood.